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(54) **Gene therapy to promote angiogenesis**

(57) The rationale for the present invention is provided by the observation that the formation of new blood vessels is increased when endothelial cells are provided with for instance VEGF, bFGF or a nitric oxide synthetase. Moreover, a surprisingly synergistic effect of the combination of nitric oxide synthetase and other angiogenesis promoting factors was found. The present invention now provides means and method for enhancing and/or inducing angiogenesis.

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Description**FIELD OF INVENTION**

- 5 [0001] The present invention relates to the field of human gene therapy, more in particular to gene therapy vehicles for the treatment of cardiovascular disease.

BACKGROUND OF THE INVENTION

- 10 [0002] Hypertension and hypercholesterolemia are two of the main risk factors for human health in the Western world; these conditions can lead to atherosclerosis. Atherosclerosis may result in a number of severe cardiovascular diseases, like chronic heart failure, angina pectoris, claudicatio intermittens, or peripheral and myocardial ischemia. At least the early phases of atherosclerosis are characterised by endothelial dysfunction. Endothelial dysfunction causes coronary arterial constriction, plays a role in both hypertension and hypercholesterolemia. It is one of the first measurable steps in the cascade of reactions leading to atherosclerosis, even before macroscopic lesions are evident. Many therapies have been investigated to assess the possibility to reverse the endothelial dysfunction, and to stimulate the formation of new blood vessels (angiogenesis). It has been suggested that oral L-arginine supplementation in the diet may be a therapeutic strategy to improve angiogenesis in patients with endothelial dysfunction.

- 20 [0003] It is well established that angiogenesis is mediated by a multitude of cytokines (like TNF- α and E-selectin) and angiogenic factors including bFGF (basic Fibroblast Growth Factor), VEGF (Vascular Endothelial Growth Factor), and TGF- β . Both bFGF and VEGF are key regulators of angiogenesis in adult tissues. They selectively stimulate proliferation of endothelial cells, starting with the binding of these growth factors to receptors present on the endothelial cell surface.

- 25 [0004] Nitric oxide (NO) has been shown to play a role in this process. NO, originally identified as endothelium-derived relaxing factor, is an important endothelial vasoactive factor.

- While both NO and angiogenic factors like bFGF and VEGF play a key role in the endothelial functions, their precise mode of action is not known. On the one hand, levels of angiogenic factors like bFGF and VEGF are increased in patients suffering from endothelial dysfunction. On the other hand, is the release of nitric oxide in vascular endothelial dysfunction often reduced. This reduced release may cause constriction of the coronary arteries and thus contribute to heart disease. It is postulated that patients suffering from endothelial dysfunction could benefit from therapies to increase new collateral blood vessel formation and/or therapies to increase vasodilation.

- 30 [0005] Many experimental gene therapies concentrate on the stimulation of angiogenesis, in patients suffering from endothelial dysfunction, through the addition of VEGF or bFGF. Though these experimental therapies may have some effect, the level of therapy induced angiogenesis is low, leading to a slow, if at all, recovery or enhancement of blood flow.

- [0006] It has been demonstrated that NO is involved in VEGF-mediated proliferation of endothelial cells. Exposure of endothelial cells to VEGF was shown to lead to the activation of constitutive NO synthase (ceNOS) and the release of biologically active NO. The proliferation of cells by VEGF can be inhibited by specific NOS-inhibitors like L-NAME, indicating that NO is an essential mediator in the VEGF-induced cell proliferation and angiogenesis.

- 40 [0007] Likewise, the presence of bFGF can increase ceNOS protein levels and enzyme activity during healing of rat gastric ulcers. Here also, the healing was inhibited specifically by the NOS-inhibitor L-NAME. In transgenic mouse models, disruption of the endogenous ceNOS gene impaired angiogenesis (Murohara et al.). This could not be compensated by the administration of VEGF, showing the essential role for NO in growth factor mediated angiogenesis.

SUMMARY OF THE INVENTION

- 45 [0008] The art teaches that NO is a secondary signal in the angiogenic response of endothelial cells to growth factors like bFGF and VEGF, and that NO acts as a downstream mediator of angiogenesis. Furthermore, the art suggests that the expression of the ceNOS gene in endothelial cells is a result of the induction by the growth factors, leading to the release of biologically active NO.

However, despite the increase in the levels of angiogenic factors like bFGF and VEGF, this does not result in sufficient collateral forming capacity.

- In one aspect of the present invention we demonstrate that at least one of the limiting factors is NO. In another aspect of the invention we demonstrate that NO levels in the arterial wall are insufficient. In another aspect the invention provides a method for increasing angiogenesis through locally increasing NO and/or endothelial growth factors such as but not limited to VEGF and/or bFGF. In yet another aspect the invention provides a method for increasing vasodilation of blood vessels. In another aspect the invention provides a method for increasing angiogenesis through locally delivering an expression vector, preferably an adenovirus vector, comprising at least an expression cassette for ceNOS, to sites

selected for being provided with the capacity to induce, or at least in part promote, angiogenesis.

BRIEF DESCRIPTION OF THE DRAWINGS

5 [0009]

Figure 1. Cell number of cultures of PER.C6 cells grown at 32, 37 or 39 degrees centigrade.

Figure 2. Western blot of different PER.C6 clones transfected with E2A125.

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Figure 3. Suspension growth characteristics of PER.C6ts125E2A C5-9 cells.

Figure 4. Mean capillary tube length of tubular structures in cultured MVEC cells infected with Ad.IG.CMV.eNOS in the presence or absence of TNF, bFGF, L-NAME and or VEGF as indicated.

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Figure 5. Photographs of MVEC cells grown in the presence of VEGF with or without MVEC cells infected with Ad.IG.CMV.NOS.

DETAILED DESCRIPTION OF THE INVENTION

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[0010] A rationale for the present invention is provided by the observation that the formation of new blood vessels in vitro cultures of human foreskin microvascular endothelial cells (MVEC) was increased through providing said cells with a sequence coding for a VEGF, a bFGF or a nitric oxide synthetase. Moreover, a surprisingly synergistic effect of the combination of a sequence coding for a nitric oxide synthetase with a sequence encoding other angiogenesis promoting factors such as VEGF, bFGF was found. This effect was unanticipated because nitric oxide is produced as a result of the exposure of endothelial cells to VEGF and/or bFGF. Since these factors promote the production of NO a lower than additional effect of extra NO was expected. One possible explanation for the observed synergistic effect is that the signal for stimulation and/or enhancement of angiogenesis by VEGF and/or bFGF triggers at least two signal transduction pathways. In at least one pathway NO is at least in part involved in continuing and/or amplifying the signal cascade, whereas in at least one other pathway, NO is not essentially involved. Both the NO comprising and the NO "independent" signal transduction pathway need to function optimally for optimal induction and/or enhancement of angiogenesis. In case of the presence of only NO, the NO "independent" is not optimally induced, whereas in case of the presence of only VEGF and/or bFGF, the NO comprising signal transduction pathway is not optimally induced. It is not known whether said pathway are completely separate. It may be that said pathways are separate in a certain part of the cascade and may join together in another part or parts of signal transduction cascade.

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[0011] In one aspect the invention provides a nucleic acid delivery vehicle for enhancing and/or inducing angiogenesis comprising nucleic acid comprising at least one sequence coding for a protein capable of increasing nitric oxide production and further comprising a nucleic acid delivery carrier. Preferably said sequence codes for a nitric oxide synthetase. Preferably said sequences codes for eNOS. In a preferred embodiment said nucleic acid delivery vehicle further comprises at least one sequence encoding an additional angiogenesis promoting factor. Preferably said additional angiogenesis promoting factor is of VEGF, bFGF or angiopoietin-1 or parts or derivatives or functional analogues thereof. Said additional angiogenesis promoting factors, necessary for obtaining a synergistic effect may be supplied by sequences provided by said nucleic acid delivery vehicle or be provided in other ways. They may also be provided by cells transduced or surrounding transduced cells. In a preferred embodiment of the invention the expression of at least one of said sequences is regulated by a signal. Preferably said signal is provided by the oxygen tension in a cell. Preferably said oxygen tension signal is translated into a different expression by a hypoxia inducible factor 1 α promoter. In another aspect of the invention said nucleic acid delivery vehicle further comprising a sequence encoding a herpes simplex virus thymidine kinase. Thus providing an additional method of regulating the level of enhanced and/or induced angiogenesis. Said level may be at least in part be reduced through the addition of gancyclovir, killing not only at least in part the dividing cells in the newly forming vessel parts, but also killing at least in part transduced cells thereby limiting the supply of nitric oxide and/or additionally angiogenesis promoting factors.

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Said nucleic acid delivery carrier may be any nucleic acid delivery carrier. In a preferred embodiment of the invention said nucleic acid delivery carrier comprises an adenovirus vector or an adeno-associated virus vector preferably including at least essential parts of adenovirus vector DNA or adeno-associated virus vector DNA. Preferably a nucleic acid delivery vehicle has been provided with a least a partial tissue tropism for muscle cells. Preferably a nucleic acid delivery vehicle has been at least in part deprived of a tissue tropism for liver cells. Preferably said tissue tropism is provided or deprived at least in part through a tissue tropism determining part of fiber protein of a subgroup B adenovirus. A preferred subgroup B adenovirus is adenovirus 16.

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In another aspect the invention provides a method for enhancing and/or inducing angiogenesis comprising providing cells of an individual with a nucleic acid delivery vehicle according to the invention and allowing said cells to grow under conditions allowing expression of a protein capable of increasing nitric oxide production. Preferably said method is a method for enhancing and/or inducing angiogenesis in a synergistic fashion with at least one additional angiogenesis promoting factor or parts or derivatives or functional analogues thereof. Preferably said enhancing and/or inducing angiogenesis effect is at least in part reversible.

Preferably, said effect is at least in part reversed through an increase in the oxygen tension or through providing said cells with gancyclovir or functional analogue thereof, or both.

In a preferred aspect the invention at least cells are transduced that under normal circumstances are not in direct contact with blood. The advantage being that in this way the treatment promotes at least in part the localisation of the effect. Preferably said cells not in direct contact with the blood are muscle cells, preferably smooth muscle cells. When feasible it a preferred means of providing cells with a nucleic acid delivery vehicle of the invention is a catheter, preferably an Infiltrator catheter (EP 97200330.5) In one aspect, the invention provides the use of a nucleic acid delivery vehicle or a method for the treatment of endothelial dysfunction. In one embodiment said use increases at least in part vasodilation of constricted vessels. In another embodiment said use increases at least in part angiogenesis, be it enhanced or induced or both.

In another aspect the invention provides a cell for the production of an adenovirus vector or an adeno-associated virus vector of the invention wherein said cell comprises a means for the production of said virus vector in the absence of replication competent adenovirus and adeno-associated virus. In a preferred embodiment said cell expresses at least one means for the production of said virus vector from a nucleic acid integrated in the chromosomal DNA of said cell and expresses other means for the production of said virus vector from nucleic acid not integrated in the chromosomal DNA of said cell and wherein said integrated nucleic acid and said non-integrated nucleic acid, do not comprise sequence overlap leading to the formation of replication competent adenovirus. In a particularly preferred embodiment said integrated nucleic acid comprises at least an adenovirus E1-region. In another particularly preferred embodiment said integrated nucleic acid comprises at least a sequence encoding an adenovirus E2A protein, preferably an E2A-protein derived from adenovirus ts125. In another preferred embodiment said integrated nucleic acid comprises an adenovirus E4-region, preferably E4-orf6.

Preferably said cell is derived from a PER.C6 cell (ECACC deposit number 96022940).

[0012] It is an object of the present invention to provide gene therapies for local administration of NO or VEGF in the arterial wall. It is also an object of the invention to induce angiogenesis in patients with endothelial dysfunction. Furthermore, it is an object of this invention to provide methods to increase NO production in the endothelium, thereby removing a cause for endothelial dysfunction.

Gene therapy vehicles and methods of application are disclosed herein, based on the expression in endothelial cells of a NO synthase sequence, alone or in combination with sequences encoding angiogenic factors like bFGF and VEGF. The synthesis of NO synthase is regulated by a family of isozymes. Three isoforms are known, nNOS, ceNOS and iNOS. Both nNOS and ceNOS are constitutively expressed and tightly regulated by calmodulin, whereas iNOS is induced by the action of cytokines.

[0013] The present invention discloses the treatment of human microvascular endothelial cells with VEGF or bFGF, resulting in capillary blood vessel formation. The invention also discloses the transfection of these cells with a NOS sequence, resulting in a strong response in capillary vessel formation. Furthermore, the invention discloses the treatment with combinations of sequences encoding NO synthase and VEGF or bFGF, resulting in a strong synergistic response in angiogenesis.

[0014] It is also an object of the present invention to provide viral vectors that contain a nitric oxide synthase (NOS) sequence, or a sequence encoding bFGF or VEGF, or combinations of these. Such viral vectors are useful in gene therapy strategies aimed at improving angiogenesis in patients with impaired endothelial function. In an embodiment of the invention, adenoviral vectors are employed to deliver these sequences. Adenoviruses are convenient viruses for construction of vectors for gene therapy, because of their high efficacy to deliver DNA in most mammalian cell types. Based on the detailed knowledge of their DNA genomes, especially of adenovirus types 2 and 5, recombinant adenoviral vectors have been developed (Bout review, 1997). The recombinant adenoviruses lack E1 sequences to prohibit replication; the recombinant virus may also carry deletion of all E2A sequences. In the present invention, vectors are provided that lack both E1 and E2A sequences, where these sequences have been replaced with either a nitric oxide synthase (NOS) transgene, a transgene encoding bFGF or VEGF, or combinations of these transgenes.

[0015] In a further embodiment of the present invention, adenoviral vectors are provided that lack the early genes E1 and E2A, the sequences of which are replaced by the transgenes. In another embodiment of the present invention, complementing cell lines are provided for packaging of such adenoviral vectors.

[0016] It is clear that when reference is made to a certain protein, that for the purpose of the invention also functional analogues or derivatives of said protein may be used, wherein said functional analogue possesses the same kind of activity though not necessarily the same amount of activity.

EXAMPLES

Example 1: THE GENERATION OF A RECOMBINANT ADENOVIRAL VECTOR EXPRESSING A ceNOS/VEGF121 GENE

5 [0017] To construct an adapter plasmid that allows the generation of a recombinant adenoviral vector expressing both the NO synthase cDNA and the cDNA for an angiogenic growth factor we have used the internal ribosome entry site (IRES) of the encephalomyocarditis virus (EMCV, Jang et al., 1988; J. Virol. 62, 2636-2643). In this example we have used the cDNA coding for the isoform VEGF₁₂₁ (Tischer et al., 1991; J. Biol. Chem. 266, 11947-11954) as the

10 angiogenic factor in the ceNOS gene. A 386 bp PCR fragment spanning the coding region for VEGF₁₂₁ was generated using total cDNA from human umbilical vein endothelial cells (total RNA isolation using Trizol procedure, first strand cDNA synthesis using the supercript II kit: Gibco BRL) as a template, and the following primers: VEGF-f: 5'-GCC TCA TGA ACT TTC TGC TGT C-3' and VEGF121-r: 5'-AAA GTC GAC TCT AGA TCA GCT CAT CTC TCC TAT CTG C-3'.

15 Pwo DNA polymerase was used according to the manufacturers protocol with the following temperature cycles: once 5' at 95°C; 3' at 55°C; 1' at 72°C; and 30 cycles of 1' at 95°C, 1' at 55°C, 1' at 72°C, followed by once 10' at 72°C. The PCR product was then digested with RcaI and Sall and purified on an LMP agarose gel (SeaPlaque GTG). pBr/PTkEM-CVNeo/2 (WO 96/35798) was digested with Sall and partially digested with NcoI to yield a vector fragment of 6866 bp that was purified on LMP agarose gel and subsequently ligated with the RcaI and Sall digested VEGF121 PCR fragment to generate pBr/PTkEMCV/VEGF121. This plasmid was digested with XbaI and a 956 bp XbaI fragment harbouring the VEGF121 DNA downstream of the EMCV IRES was purified and cloned into XbaI site of the pAd/CLIP:ceNOS adapter plasmid. The resulting adapter plasmid pAd/CLIP:ceNOS/VEGF121 has the ceNOS cDNA immediately downstream of the CMV promoter, followed by the IRES, followed by the VEGF121 cDNA. Recombinant adenoviral vectors derived from the pAd/CLIP:ceNOS/VEGF121 introduce a bicistronic mRNA in the infected cells that is transcribed from the CMV promoter and facilitates the translation of both NO synthase and VEGF₁₂₁.

25 EXAMPLE 2: GENERATION OF PRODUCER CELL LINES FOR THE PRODUCTION OF RECOMBINANT ADENOVIRAL VECTORS DELETED IN EARLY REGION 1 AND EARLY REGION 2A

[0018] This example describes the generation of cell lines for the production of recombinant adenoviral vectors that are deleted in early region 1 (E1) and early region 2A (E2A). The producer cell lines complement for the E1 and E2A deletion from recombinant adenoviral vectors in trans by constitutive expression of the E1 and E2A genes, respectively. The pre-established Ad5-E1 transformed human embryo retinoblast cell line PER.C6 (WO 97/00326) and Ad5 transformed human embryo kidney cell line 293 (Graham, 1977) were further equipped with E2A expression cassettes. The adenoviral E2A gene encodes a 72 kDa DNA Binding Protein (DBP) which has a high affinity for single stranded

35 DNA. Because of this feature, constitutive expression of DBP is toxic for cells. The ts125E2A mutant encodes a DBP which has a Pro→Ser substitution of amino acid 413 (van der Vliet, 1975). Due to this mutation, the ts125E2A encoded DBP is fully active at the permissive temperature of 32°C, but does not bind to ssDNA at the non-permissive temperature of 39°C. This allows the generation of cell lines that constitutively express E2A which is not functional and is not toxic at the non-permissive temperature of 39°C, but becomes functional after a temperature switch to the permissive

40 temperature of 32°C.

Example 2A. Generation of plasmids expressing wildtype E2A-or temperature sensitive ts125E2A.

[0019] pcDNA3wtE2A: The complete wildtype early region 2A (E2A) coding region was amplified from the plasmid pBR/Ad.Bam-rITR (ECACC deposit P97082122) with the primers DBPpcr1 and DBPpcr2 using the ExpandTM Long Template PCR system according to the standard protocol of the supplier (Boehringer Mannheim). PCR was performed on a Biometra Trio Thermoblock, amplification program: 94°C for 2 minutes, 1 cycle; 94°C for 10 seconds + 51°C for 30 seconds + 68°C for 2 minutes, 1 cycle; 94°C for 10 seconds + 58°C for 30 seconds + 68°C for 2 minutes, 10 cycles; 94°C for 10 seconds + 58°C for 30 seconds + 68°C for 2 minutes with 10 seconds extension per cycle, 20 cycles; 68°C

50 for 5 minutes, 1 cycle. The primer DBPpcr1: CGG GAT CCG CCA CCA TGG CCA GTC GGG AAG AGG AG (5' to 3') contains a unique BamHI restriction site (underlined) 5' of the Kozak sequence (italic) and start codon of the E2A coding sequence. The primer DBPpcr2: CGG PAT TCT TAA AAA TCA AAG GGG TTC TGC CGC (5' to 3') contains a unique EcoRI restriction site (underlined) 3' of the stop codon of the E2A coding sequence. The bold characters refer to sequences derived from the E2A coding region. The PCR fragment was digested with BamHI/EcoRI and cloned into BamHI/EcoRI digested pcDNA3 (Invitrogen), giving rise to pcDNA3wtE2A.

55 [0020] pcDNA3tsE2A: The complete ts125E2A coding region was amplified from DNA isolated from the temperature sensitive adenovirus mutant H5ts125 (Ensinger and Ginsberg, 1972; van der Vliet, 1975). The PCR amplification procedure was identical to that for the amplification of wtE2A. The PCR fragment was digested with BamHI/EcoRI and

cloned into BamHI/EcoRI digested pcDNA3 (Invitrogen), giving rise to pcDNA3tsE2A. The integrity of the coding sequence of wtE2A and tsE2A was confirmed by sequencing.

Example 2B. Growth characteristics of producer cells for the production of recombinant adenoviral vectors cultured at 32-, 37- and 39°C.

[0021] PER.C6 cells were cultured in Dulbecco's Modified Eagle Medium (DMEM, Gibco BRL) supplemented with 10% Foetal Bovine Serum (FBS, Gibco BRL) and 10mM MgCl₂ in a 10% CO₂ atmosphere at either 32°C, 37°C or 39°C. At day 0, a total of 1×10^6 PER.C6 cells were seeded per 25cm² tissue culture flask (Nunc) and the cells were cultured at either 32°C, 37°C or 39°C. At day 1-8, cells were counted. Figure 1 shows that the growth rate and the final cell density of the PER.C6 culture at 39°C is comparable to that at 37°C. The growth rate and final density of the PER.C6 culture at 32°C were slightly reduced as compared to that at 37°C or 39°C. No significant cell death was observed at any of the incubation temperatures. Thus PER.C6 performs very well both at 32°C and 39°C, the permissive and non-permissive temperature for ts125E2A, respectively.

Example 2C. Transfection of PER.C6 and 293 with E2A expression vectors; colony formation and generation of cell lines

[0022] One day prior to transfection, 2×10^6 PER.C6 cells were seeded per 6 cm tissue culture dish (Greiner) in DMEM, supplemented with 10% FBS and 10mM MgCl₂ and incubated at 37°C in a 10% CO₂ atmosphere. The next day, the cells were transfected with 3-, 5- or 8µg of either pcDNA3, pcDNA3wtE2A or pcDNA3tsE2A plasmid DNA per dish, using the LipofectAMINE PLUS™ Reagent Kit according to the standard protocol of the supplier (Gibco BRL), except that the cells were transfected at 39°C in a 10% CO₂ atmosphere. After the transfection, the cells were constantly kept at 39°C, the non-permissive temperature for ts125E2A. Three days later, the cells were put on DMEM, supplemented with 10% FBS, 10mM MgCl₂ and 0.25mg/ml G418 (Gibco BRL) and the first G418 resistant colonies appeared at 10 days post transfection. As shown in table 1, there was a dramatic difference between the total number of colonies obtained after transfection of pcDNA3 (~200 colonies) or pcDNA3tsE2A (~100 colonies) and pcDNA3wtE2A (only 4 colonies). These results indicate that the toxicity of constitutively expressed E2A can be overcome by using a temperature sensitive mutant of E2A (ts125E2A) and culturing of the cells at the non-permissive temperature of 39°C.

[0023] From each transfection, a number of colonies was picked by scraping the cells from the dish with a pipette. The detached cells were subsequently put into 24 wells tissue culture dishes (Greiner) and cultured further at 39°C in a 10% CO₂ atmosphere in DMEM, supplemented with 10% FBS, 10mM MgCl₂ and 0.25mg/ml G418. As shown in table 1, 100% of the pcDNA3 transfected colonies (4/4) and 82% of the pcDNA3tsE2A transfected colonies (37/45) were established to stable cell lines (the remaining 8 pcDNA3tsE2A transfected colonies grew slowly and were discarded). In contrast, only 1 pcDNA3wtE2A transfected colony could be established. The other 3 died directly after picking.

[0024] Next, the E2A expression levels in the different cell lines were determined by Western blotting. The cell lines were seeded on 6 well tissue culture dishes and sub-confluent cultures were washed twice with PBS (NPBI) and lysed and scraped in RIPA (1% NP-40, 0.5% sodium deoxycholate and 0.1% SDS in PBS, supplemented with 1mM phenylmethylsulfonylfluoride and 0.1 mg/ml trypsin inhibitor). After 15 minutes incubation on ice, the lysates were cleared by centrifugation. Protein concentrations were determined by the Bio-Rad protein assay, according to standard procedures of the supplier (BioRad). Equal amounts of whole-cell extract were fractionated by SDS-PAGE on 10% gels. Proteins were transferred onto Immobilon-P membranes (Millipore) and incubated with the αDBP monoclonal antibody B6 (Reich, 1983). The secondary antibody was a horseradish-peroxidase conjugated goat anti mouse antibody (BioRad). The Western blotting procedure and antibody incubations were performed according to the protocol provided by Millipore. The antibody complexes were visualised with the ECL detection system according to the manufacturer's protocol (Amersham). Figure 2 shows that all of the cell lines derived from the pcDNA3tsE2A transfection express the 72-kDa E2A protein (upper panel, lanes 4-14; middle panel, lanes 1-13; lower panel, lanes 1-12). In contrast, the only cell line derived from the pcDNAwtE2A transfection did not express the E2A protein (lane 2). No E2A protein was detected in extract from a cell line derived from the pcDNA3 transfection (lane 1), which serves as a negative control. Extract from PER.C6 cells transiently transfected with pcDNA3ts125 (lane 3) served as a positive control for the Western blot procedure. These data confirm that constitutive expression of wtE2A is toxic for cells and that this toxicity can be circumvented by using the ts125 mutant of E2A.

[0025] In contrast to PER.C6 cells, the culturing of 293 cells at 39°C is troublesome. Therefore, the transfection of 293 cells with either pcDNA3, pcDNA3wtE2A or pcDNA3tsE2A was performed at 37°C in an atmosphere of 10% CO₂, a semi-permissive temperature for ts125E2A encoded DBP. A day prior to transfection, 293 cells were seeded in, supplemented with 10% FBS and 10mM MgCl₂, at a density of 3.6×10^5 cells per 6 cm tissue culture dish (Greiner). Five hours before transfection, cells received fresh medium. Cells were transfected with 7.2µg of either pcDNA3, pcDNA3wtE2A or pcDNA3tsE2A plasmid DNA using the Calcium Phosphate Transfection System according to the

standard protocol of the supplier (Gibco BRL). Two days post transfection, cells were put on selection medium, i.e. DMEM supplemented with 10% FBS, 10mM MgCl₂ and 0.1 mg/ml G418. The first colonies appeared at day 12 post transfection. The total number of colonies obtained after transfection of pcDNA3 (~100 colonies) or pcDNA3tsE2A (~25 colonies) was significantly higher than that obtained after transfection of pcDNA3wtE2A (only 2 colonies). These results again show that constitutively expressed E2A is toxic for cells and that this toxicity can be circumvented by using ts125E2A. Moreover, it shows that this is not specific for PER.C6 cells, but that it applies to eukaryotic cells in general (e.g. 293 cells).

Example 2D. Complementation of the E2A deletion in Ad5.dl802 by PER.C6 cells constitutively expressing ts125E2A.

[0026] The adenovirus Ad5.dl802 is an Ad 5 derived vector deleted for the major part of the E2A coding region and does not produce functional DBP (Rice, 1985). Ad5.dl802 was used to test the E2A trans-complementing activity of PER.C6 cells constitutively expressing ts125E2A. Parental PER.C6 cells or PER.C6tsE2A clone 3-9 were cultured in DMEM, supplemented with 10% FBS and 10mM MgCl₂ at 39°C and 10% CO₂ in 25 cm² flasks and either mock infected or infected with Ad5.dl802 at an m.o.i. of 5. Subsequently the infected cells were cultured at 32°C and cells were screened for the appearance of a cytopathic effect (CPE) as determined by changes in cell morphology and detachment of the cells from the flask. Table 2 shows that full CPE appeared in the Ad5.dl802 infected PER.C6tsE2A clone 3-9 within 2 days. No CPE appeared in the Ad5.dl802 infected PER.C6 cells or the mock infected cells. These data show that PER.C6 cells constitutively expressing ts125E2A complement in trans for the E2A deletion in the Ad5.dl802 vector at the permissive temperature of 32°C.

EXAMPLE 3: SERUM FREE SUSPENSION CULTURE OF PER.C6TSE2A CELL LINES.

[0027] Large scale production of recombinant adenoviral vectors for human gene therapy requires an easy and upscalable culturing method for the producer cell line, preferably a suspension culture, in medium devoid of any human or animal constituents. To that end, the cell line PER.C6tsE2A c5-9 (designated c5-9) was cultured at 39°C and 10% CO₂ in a 175 cm² tissue culture flask (Nunc) in DMEM, supplemented with 10% FBS and 10mM MgCl₂. At sub-confluency (70-80% confluent), the cells were washed with PBS (NPBI) and the medium was replaced by 25 ml serum free suspension medium Ex-cell™ 525 (JRH) supplemented with 1 x L-Glutamin (Gibco BRL), hereafter designated SFM. Two days later, cells were detached from the flask by flicking and the cells were centrifuged at 1000rpm for 5 minutes. The cell pellet was resuspended in 5 ml SFM and 0.5ml cell suspension was transferred to a 80 cm² tissue culture flask (Nunc), together with 12 ml fresh SFM. After 2 days, cells were harvested (all cells are in suspension) and counted in a Burkert cell counter. Next, the cells were seeded in a 125ml tissue culture erlenmeyer (Corning) at a seeding density of 3 x 10⁵ cells per ml in a total volume of 20 ml SFM. Cells were further cultured at 125 RPM on an orbital shaker (GFL) at 39°C in a 10% CO₂ atmosphere. Cells were counted at day 1-6 in a Burkert cell counter. In Figure 3, the mean growth curve from 8 cultures is shown. PER.C6tsE2A c5-9 performs well in serum free suspension culture. The maximum cell density of approximately 2 x 10⁶ cells per ml is reached within 5 days of culture.

EXAMPLE 4: PLASMID BASED SYSTEM FOR THE GENERATION OF RECOMBINANT ADENOVIRAL VECTORS DELETED IN EARLY REGION 1 AND EARLY REGION 2A

Example 4A. Generation of pBr/Ad.Bam-rlTR (ECACC deposit P97082122)

[0028] In order to facilitate blunt end cloning of the ITR sequences, wild-type human adenovirus type 5 (Ad5) DNA was treated with Klenow enzyme in the presence of excess dNTPs. After inactivation of the Klenow enzyme and purification by phenol/chloroform extraction followed by ethanol precipitation, the DNA was digested with BamHI. This DNA preparation was used without further purification in a ligation reaction with pBr322 derived vector DNA prepared as follows: pBr322 DNA was digested with EcoRV and BamHI, dephosphorylated by treatment with TSAP enzyme (Life Technologies) and purified on LMP agarose gel (SeaPlaque GTG). After transformation into competent E. coli DH5a (Life Techn.) and analysis of ampicillin resistant colonies, one clone was selected that showed a digestion pattern as expected for an insert extending from the BamHI site in Ad5 to the right ITR. Sequence analysis of the cloning border at the right ITR revealed that the most 3' G residue of the ITR was missing, the remainder of the ITR was found to be correct. Said missing G residue is complemented by the other ITR during replication.

Example 4B. Generation of pBr/Ad.Sal-rITR (ECACC deposit P97082119)

[0029] pBr/Ad.Bam-rITR was digested with BamHI and Sall. The vector fragment including the adenovirus insert was isolated in LMP agarose (SeaPlaque GTG) and ligated to a 4.8 kb Sall-BamHI fragment obtained from wt Ad5 DNA and purified with the GeneClean II kit (Bio 101, Inc.). One clone was chosen and the integrity of the Ad5 sequences was determined by restriction enzyme analysis. Clone pBr/Ad.Sal-rITR contains adeno type 5 sequences from the Sall site at bp 16746 up to and including the rITR (missing the most 3' G residue).

Example 4C. Generation of pBr/Ad.AflII-Bam (ECACC deposit P97082114)

[0030] First pBr/Ad.Cla-Bam (ECACC deposit P97082117) was generated. Wt Adeno type 5 DNA was digested with ClaI and BamHI, and the 20.6 kb fragment was isolated from gel by electroelution. pBr322 was digested with the same enzymes and purified from agarose gel by GeneClean. Both fragments were ligated and transformed into competent DH5 α . The resulting clone pBr/Ad.Cla-Bam was analysed by restriction enzyme digestion and shown to contain an insert with adenovirus sequences from bp 919 to 21566. Next pBr/Ad.Cla-Bam was linearised with EcoRI (in pBr322) and partially digested with AflII. After heat inactivation of AflII for 20' at 65 °C the fragment ends were filled in with Klenow enzyme. The DNA was then ligated to a blunt double stranded oligo linker containing a PacI site (5'-AATTGCTCTAATTAACCGCTTAA-3'). This linker was made by annealing the following two oligonucleotides: 5'-AATTGCTCTTAATTAACCGC-3' and 5'-AATTGCGTTAATTAAGAC-3', followed by blunting with Klenow enzyme. After precipitation of the ligated DNA to change buffer, the ligations were digested with an excess PacI enzyme to remove concatamers of the oligo. The 22016 bp partial fragment containing Ad5 sequences from bp 3534 up to 21566 and the vector sequences, was isolated in LMP agarose (SeaPlaque GTG), religated and transformed into competent DH5 α . One clone that was found to contain the PacI site and that had retained the large adeno fragment was selected and sequenced at the 5' end to verify correct insertion of the PacI linker in the (lost) AflII site.

Example 4D. Generation of pBr/Ad.Bam-rITRpac#2 (ECACC deposit P97082120) and pBr/Ad.Bam-rITR#8 (ECACC deposit P97082121)

[0031] To allow insertion of a PacI site near the ITR of Ad5 in clone pBr/Ad.Bam-rITR about 190 nucleotides were removed between the ClaI site in the pBr322 backbone and the start of the ITR sequences. This was done as follows: pBr/Ad.Bam-rITR was digested with ClaI and treated with nuclease Bal31 for varying lengths of time (2', 5', 10' and 15'). The extend of nucleotide removal was followed by separate reactions on pBr322 DNA (also digested at the ClaI site), using identical buffers and conditions. Bal31 enzyme was inactivated by incubation at 75 °C for 10', the DNA was precipitated and resuspended in a smaller volume TE buffer. To ensure blunt ends, DNAs were further treated with T4 DNA polymerase in the presence of excess dNTPs. After digestion of the (control) pBr322 DNA with Sall, satisfactory degradation (~150 bp) was observed in the samples treated for 10' or 15'. The 10' or 15' treated pBr/Ad.Bam-rITR samples were then ligated to the above described blunted PacI linkers (See pBr/Ad.AflII-Bam). Ligations were purified by precipitation, digested with excess PacI and separated from the linkers on an LMP agarose gel. After religation, DNAs were transformed into competent DH5 α and colonies analysed. Ten clones were selected that showed a deletion of approximately the desired length and these were further analysed by T-track sequencing (T7 sequencing kit, Pharmacia Biotech). Two clones were found with the PacI linker inserted just downstream of the rITR. After digestion with PacI, clone #2 has 28 bp and clone #8 has 27 bp attached to the ITR.

Example 4E. Generation of pWE/Ad.AflII-rITR (ECACC deposit P97082116)

[0032] Cosmid vector pWE15 (Clontech) was used to clone larger Ad5 inserts. First, a linker containing a unique PacI site was inserted in the EcoRI sites of pWE15 creating pWE.pac. To this end, the double stranded PacI oligo as described for pBr/Ad.AflII-BamHI was used but now with its EcoRI protruding ends. The following fragments were then isolated by electroelution from agarose gel: pWE.pac digested with PacI, pBr/AflII-Bam digested with PacI and BamHI and pBr/Ad.Bam-rITR#2 digested with BamHI and PacI. These fragments were ligated together and packaged using λ phage packaging extracts (Stratagene) according to the manufacturer's protocol. After infection into host bacteria, colonies were grown on plates and analysed for presence of the complete insert. pWE/Ad.AflII-rITR contains all adenovirus type 5 sequences from bp 3534 (AflII site) up to and including the right ITR (missing the most 3' G residue).

Example 4F. Generation of pWE/Ad.AflII-EcoRI

[0033] pWE.pac was digested with ClaI and 5' protruding ends were filled using Klenow enzyme. The DNA was then digested with PacI and isolated from agarose gel. pWE/AflII-rITR was digested with EcoRI and after treatment with

Klenow enzyme digested with PacI. The large 24 kb fragment containing the adenoviral sequences was isolated from agarose gel and ligated to the ClaI-digested and blunted pWE.pac vector using the Ligation Express™ kit from Clontech. After transformation of Ultracompetent XL10-Gold cells from Stratagene, clones were identified that contained the expected insert. pWE/AfIII-EcoRI contains Ad5 sequences from bp 3534-27336.

Example 4G. Generation of pWE/Ad.AfIII-rITRΔE2A:

[0034] Deletion of the E2A coding sequences from pWE/Ad.AfIII-rITR (ECACC deposit P97082116) has been accomplished as follows. The adenoviral sequences flanking the E2A coding region at the left and the right site were amplified from the plasmid pBr/Ad.Sal.rITR (ECACC deposit P97082119) in a PCR reaction with the Expand PCR system (Boehringer) according to the manufacturers protocol. The following primers were used:

Right flanking sequences (corresponding Ad5 nucleotides 24033 to 25180):

[0035]

ΔE2A.SnaBI: 5'-GGC GTA CGT AGC CCT GTC GAA AG-3'

ΔE2A.DBP-start: 5'-CCA ATG CAT TCG AAG TAC TTC CTT CTC CTA TAG GC-3'

[0036] The amplified DNA fragment was digested with SnaBI and NsiI (NsiI site is generated in the primer ΔE2A.DBP-start, underlined).

Left flanking sequences (corresponding Ad5 nucleotides 21557 to 22442):

[0037]

ΔE2A.DBP-stop: 5'-CCA ATG CAT ACG GCG CAG ACG G-3'

ΔE2A.BamHI: 5'-GAG GTG GAT CCC ATG GAC GAG-3'

[0038] The amplified DNA was digested with BamHI and NsiI (NsiI site is generated in the primer ΔE2A.DBP-stop, underlined).

[0039] Subsequently, the digested DNA fragments were ligated into SnaBI/BamHI digested pBr/Ad.Sal-rITR. Sequencing confirmed the exact replacement of the DBP coding region with a unique NsiI site in plasmid pBr/Ad.Sal-rITRΔE2A. The unique NsiI site can be used to introduce an expression cassette for a gene to be transduced by the recombinant vector.

Next, the plasmid pWE/Ad.AfIII-rITRΔE2A was generated. The plasmid pBr/Ad.Sal-rITRΔE2A was digested with BamHI and SpeI. The 3.9 Kb fragment in which the E2A coding region was replaced by the unique NsiI site was isolated. The pWE/Ad.AfIII-rITR was digested with BamHI and SpeI. The 35 Kb DNA fragment, from which the BamHI/SpeI fragment containing the E2A coding sequence was removed, was isolated. The fragments were ligated and packaged using λ phage packaging extracts according to the manufacturers protocol (Stratagene), yielding the plasmid pWE/Ad.AfIII-rITRΔE2A.

Example 4H. Generation of the adapter plasmids

[0040] Adapter plasmid pMLPTK (patent application EP 95202213) was modified as follows: SV40 polyA sequences were amplified with primer SV40-1 (introduces a BamHI site) and SV40-2 (introduces a BglII site). In addition, Ad5 sequences present in this construct (from nt. 2496 to nt. 2779; Ad5 sequences nt. 3511 to 3794) were amplified with primers Ad5-1 (introduces a BglII site) and Ad5-2.

SV40-1: 5'-GGGGGATCCGAACTTGTTTATTGCAGC-3'

SV40-2: 5'-GGGAGATCTAGACATGATAAGATAC-3'

Ad5-1: 5'-GGGAGATCTGTACTGAAATGTGTGGGC-3'

Ad5-2: 5'-GGAGGCTGCAGTCTCCAACGGCGT-3'

[0041] Both PCR fragments were digested with BglII and ligated. The ligation product was amplified with primers SV40-1 and Ad5-2 and digested with BamHI and AfIII. The digested fragment was then ligated into pMLP.TK predigested with the same enzymes. The resulting construct, named pMLP.TK, contains a deletion in adenovirus E1 sequences from nt. 459 to nt. 3510. This plasmid was used as the starting material to make a new vector in which

nucleic acid molecules comprising specific promoter and gene sequences can be easily exchanged. First, a PCR fragment was generated from pZipΔMo+PyF101(N⁺) template DNA (described in PCT/NL96/00195) with the following primers: LTR-1: 5'-CTG TAC GTA CCA GTG CAC TGG CCT AGG CAT GGA AAA ATA CAT AAC TG-3' and LTR-2: 5'-GCG GAT CCT TCG AAC CAT GGT AAG CTT GGT ACC GCT AGC GTT AAC CGG GCG ACT CAG TCA ATC G-3'. Two DNA polymerase (Boehringer Mannheim) was used according to manufacturers protocol with the following temperature cycles: once 5' at 95°C; 3' at 55°C; and 1' at 72°C, and 30 cycles of 1' at 95°C, 1' at 60°C, 1' at 72°C, followed by once 10' at 72 °C. The PCR product was then digested with BamHI and ligated into pMLP10 (Levrero et al., 1991; Gene 101, 195-202) digested with PvuII and BamHI, thereby generating vector pLTR10. This vector contains adenoviral sequences from bp 1 up to bp 454 followed by a promoter consisting of a part of the Mo-MuLV LTR having its wild-type enhancer sequences replaced by the enhancer from a mutant polyoma virus (PyF101). The promoter fragment was designated L420. Sequencing confirmed correct amplification of the LTR fragment however the most 5' bases in the PCR fragment were missing so that the PvuII site was not restored. Next, the coding region of the murine HSA gene was inserted. pLTR10 was digested with BstBI followed by Klenow treatment and digestion with NcoI. The HSA gene was obtained by PCR amplification on pUC18-HSA (Kay et al., 1990; J. Immunol. 145, 1952-1959) using the following primers: HSA1, 5'-GCG CCA CCA TGG GCA GAG CGA TGG TGG C-3' and HSA2, 5'-GTT AGA TCT AAG CTT GTC GAC ATC GAT CTA CTA ACA GTA GAG ATG TAG AA-3'. The 269 bp amplified fragment was subcloned in a shuttle vector using the NcoI and BglII sites. Sequencing confirmed incorporation of the correct coding sequence of the HSA gene, but with an extra TAG insertion directly following the TAG stop codon. The coding region of the HSA gene, including the TAG duplication was then excised as a NcoI(sticky)-Sall(blunt) fragment and cloned into the 3.5 kb NcoI(sticky)/BstBI(blunt) fragment from pLTR-10, resulting in pLTR-HSA10. Finally, pLTR-HSA10 was digested with EcoRI and BamHI after which the fragment containing the left ITR, packaging signal, L420 promoter and HSA gene was inserted into vector pMLPI.TK digested with the same enzymes and thereby replacing the promoter and gene sequences. This resulted in the new adapter plasmid pAd5/L420-HSA that contains convenient recognition sites for various restriction enzymes around the promoter and gene sequences. SnaBI and AvrII can be combined with HpaI, NheI, KpnI, HindIII to exchange promoter sequences, while the latter sites can be combined with the ClaI or BamHI sites 3' from HSA coding region to replace genes in this construct.

[0042] Another adapter plasmid that was designed to allow easy exchange of nucleic acid molecules was made by replacing the promoter, gene and poly A sequences in pAd5/L420-HSA with the CMV promoter, a multiple cloning site, an intron and a poly-A signal. For this purpose, pAd/L420-HSA was digested with AvrII and BglII followed by treatment with Klenow to obtain blunt ends. The 5.1 kb fragment with pBr322 vector and adenoviral sequences was isolated and ligated to a blunt 1570 bp fragment from pcDNA1/amp (Invitrogen) obtained by digestion with HhaI and AvrII followed by treatment with T4 DNA polymerase. This adapter plasmid was named pAd5/Clip. To enable removal of vector sequences from the adenoviral fragment pAd5/Clip was partially digested with EcoRI and the linear fragment was isolated. An oligo of the sequence 5' TTAAGTCGAC-3' was annealed to itself resulting in a linker with a Sall site and EcoRI overhang. The linker was ligated to the partially digested pAd5/Clip vector and clones were selected that had the linker inserted in the EcoRI site 23 bp upstream of the left adenovirus ITR in pAd5/Clip resulting in pAd5/Clipsal.

EXAMPLE 5: GENERATION OF RECOMBINANT ADENOVIRUSES

40 Example 5A. E1-deleted recombinant adenoviruses with wt E3 sequences

[0043] To generate E1 deleted recombinant adenoviruses with the plasmid-based system, the following constructs are prepared:

- 45 An adapter construct containing the expression cassette with the gene of interest linearised with a restriction enzyme that cuts at the 3' side of the overlapping adenoviral genome fragment, preferably not containing any pBr322 vector sequences, and
- A complementing adenoviral genome construct pWE/Ad.AfIII-rITR digested with PacI.

50 These two DNA molecules are further purified by phenol/chloroform extraction and EtOH precipitation. Co-transfection of these plasmids into an adenovirus packaging cell line, preferably a cell line according to the invention, generates recombinant replication deficient adenoviruses by a one-step homologous recombination between the adapter and the complementing construct.

[0044] A general protocol as outlined below and meant as a non-limiting example of the present invention has been performed to produce several recombinant adenoviruses using various adapter plasmids and the Ad.AfIII-rITR fragment. Adenovirus packaging cells (PER.C6) were seeded in ~25 cm² flasks and the next day when they were at ~80% confluency, transfected with a mixture of DNA and lipofectamine agent (Life Techn.) as described by the manufacturer. Routinely, 40 μl lipofectamine, 4 μgr adapter plasmid and 4 μgr of the complementing adenovirus genome fragment

Afill-rITR (or 2 µgr of all three plasmids for the double homologous recombination) are used. Under these conditions transient transfection efficiencies of ~50% (48 hrs post transfection) are obtained as determined with control transfections using a pAd/CMV-LacZ adapter. Two days later, cells are passaged to ~80 cm² flasks and further cultured. Approximately five (for the single homologous recombination) to eleven days (for the double homologous recombination) later a cytopathic effect (CPE) is seen, indicating that functional adenovirus has formed. Cells and medium are harvested upon full CPE and recombinant virus is released by freeze-thawing. An extra amplification step in a 80 cm² flask is routinely performed to increase the yield since at the initial stage the titers are found to be variable despite the occurrence of full CPE. After amplification, viruses are harvested and plaque purified on PER.C6 cells. Individual plaques are tested for viruses with active transgenes.

10 [0045] Until now, four different recombinant adenoviruses, comprising the human interleukin-3 gene, the human endothelial nitric oxide gene, the Tc1A transposase gene, or the bacterial LacZ gene, have been produced using this protocol. In all cases, functional adenovirus was formed and all isolated plaques contained viruses with an active transgene.

15 Example 5B: E1-deleted recombinant adenoviruses with modifications in the E2A, E3 and/or E4 regions

[0046] Besides replacements in the E1 region, it is possible to delete or replace the E2A region in the adenovirus. This creates the opportunity to use a larger insert or to insert more than one gene without exceeding the maximum packagable size (approximately 105% of wt genome length).

20 Recombinant viruses that are both E1 and E2A deleted are generated by a homologous recombination procedure as described above for E1-replacement vectors using a plasmid-based system consisting of:

an adapter plasmid for E1 replacement according to the invention, with or without insertion of a first gene of interest.

25 the pWE/Ad.Afill-rITRΔE2A fragment, with or without insertion of a second gene of interest.

Generation and propagation of such a virus, requires a complementing cell line for complementation of both E1 and E2A proteins in trans, as described above.

In addition to replacements in the E1 and E2A region, it is also possible to delete or replace (part of) the E3 region in the E1-deleted adenoviral vector, because E3 functions are not necessary for the replication, packaging and infection of the (recombinant) virus. This creates the opportunity to use larger inserts or to insert more than one gene without exceeding the maximum packagable size (approximately 105% of wt genome length). This can be done, e.g., by deleting part of the E3 region in the pBr/Ad.Bam-rITR clone by digestion with XbaI and religation. This removes Ad5 wt sequences 28592-30470 including all known E3 coding regions. Another example is the precise replacement of the coding region of gp19K in the E3 region with a polylinker allowing insertion of new sequences. This, 1) leaves all other coding regions intact and 2) obviates the need for a heterologous promoter since the transgene is driven by the E3 promoter and pA sequences, leaving more space for coding sequences.

To this end, the 2.7 kb EcoRI fragment from wt Ad5 containing the 5' part of the E3 region was cloned into the EcoRI site of pBluescript (KS⁺) (Stratagene). Next, the HindIII site in the polylinker was removed by digestion with EcoRV and HincII and subsequent religation. The resulting clone pBS.Eco-Eco/ad5ΔHIII was used to delete the gp19K coding region. Primers 1 (5'-GGG TAT TAG GCC AA AGG CGC A-3') and 2 (5'-GAT CCC ATG GAA GCT TGG GTG GCG ACC CCA GCG-3') were used to amplify a sequence from pBS.Eco-Eco/ad5ΔHIII corresponding to sequences 28511 to 28734 in wt Ad5 DNA. Primers 3 (5'-GAT CCC ATG GGG ATC CTT TAC TAA GTT ACA AAG CTA-3') and 4 (5'-GTC GCT GTA GTT GGA CTG G-3') were used on the same DNA to amplify Ad5 sequences from 29217 to 29476. The two resulting PCR fragments were ligated together by virtue of the new introduced NcoI site and subsequently digested with XbaI and MnlI. This fragment was then ligated into the pBS.Eco-Eco/ad5 ΔHIII vector that was digested with XbaI (partially) and MnlI generating pBS.Eco-Eco/ad5ΔHIII.Δgp19K. To allow insertion of foreign genes into the HindIII and BamHI site, an XbaI deletion was made in pBS.Eco-Eco/ad5ΔHIII.Δgp19K to remove the BamHI site in the Bluescript polylinker. The resulting plasmid pBS.Eco-Eco/ad5ΔHIIIΔgp19KΔXbaI, contains unique HindIII and BamHI sites corresponding to sequences 28733 (HindIII) and 29218 (BamHI) in Ad5. After introduction of a foreign gene into these sites, either the deleted XbaI fragment is re-introduced, or the insert is recloned into pBS.Eco-Eco/ad5ΔHIII.Δgp19K using HindIII and for example MnlI. Using this procedure, we have generated plasmids expressing HSV-TK, hIL-1α, rat IL-3, luciferase or LacZ. The unique SrfI and NotI sites in the pBS.Eco-Eco/ad5ΔHIII.Δgp19K plasmid (with or without inserted gene of interest) are used to transfer the region comprising the gene of interest into the corresponding region of pBr/Ad.Bam-rITR, yielding construct pBr/Ad.Bam-rITRΔgp19K (with or without inserted gene of interest). This construct is used as described supra to produce recombinant adenoviruses. In the viral context, expression of inserted genes is driven by the adenovirus E3 promoter.

[0047] Recombinant viruses that are both E1 and E3 deleted are generated by a double homologous recombina-

tion procedure for E1-replacement vectors using a plasmid-based system consisting of:

- an adapter plasmid for E1 replacement according to the invention, with or without insertion of a first gene of interest,
- 5 the pWE/Ad.AflII-EcoRI fragment, and
- the pBr/Ad.Bam-riTRΔgp19K plasmid with or without insertion of a second gene of interest.

- [0048] In addition to manipulations in the E3 region, changes of (parts of) the E4 region can be accomplished easily in pBr/Ad.Bam-riTR. Moreover, combinations of manipulations in the E3 and/or E2A and/or E4 region can be made.
- 10 Generation and propagation of such vectors, however, demands packaging cell lines that complement for E2A and/or E4 in trans.

EXAMPLE 6: ANGIOGENESIS ASSAY

- 15 [0049] Human foreskin microvascular endothelial cells (MVEC) were grown to confluency in M199 medium supplemented with 10% human serum (HS), 10 % new-born calf serum (NBCS), penicillin and streptomycin and infected with 3.10. pfu/ml Ad.IG.CMV.eNOS for 1 hour in M199 +2% NBCS. Medium was refreshed and cells were incubated overnight in M199+10% HS+10% NBCS.

- Angiogenesis was analysed as described in Koolwijk et al. J. Cell Biol. 132 p1177-1188 (1996). Briefly, highly confluent
- 20 MVEC were detached, seeded in a 1.25:1 split ratio on human fibrin matrices as cultures consisting either of uninfected cells, 100% infected cells or mixed cultures consisting of 10% infected/90% uninfected cells and cultured in M199 medium supplemented with 10% human serum (HS), 10% new-born calf serum (NBCS), penicillin and streptomycin.

- [0050] Invading cells and the formation of tubular structures of endothelial cells in the three-dimensional fibrin matrix were analysed by phase contrast microscopy. After 7 days the total length of the tube-like structures of six randomly chosen microscopic fields per well (7.3 mm²/field = 43.8% of the total well) was measured using a Nikon FXA
- 25 microscope equipped with a monochrome CCD camera (MX5) connected to a computer with Optimas image analysis software, and expressed as total tube length/cm².

- [0051] Part of the Ad.IG.CMV.eNOS infected MVEC cells was used to analyse the NOS activity. NOS activity was analysed by measuring the conversion of L⁻¹-C-Arginine to L⁻¹-C-Citrulline, the so-called citrulline assay.

- 30 [0052] For the angiogenesis experiments incubations are performed with cultures of uninfected cells, 10% infected MVEC and of 100% infected MVEC.

All incubations have been performed in the presence of 1 ng/ml TNF-α. Specific conditions tested in the presence and absence of virus were control, +bFGF: 5 ng/ml, +VEGF: 25 ng/ml, +bFGF+L-NAME: 5 ng/ml, 100iM

35 EXAMPLE 7: EFFECT OF ADENOVIRUSES ON ANGIOGENESIS

- [0053] The NOS activity in Ad.IG.CMV.eNOS infected MVEC, expressed as dpm L⁻¹-C-citrulline, was 3937 dpm versus 3703 dpm in uninfected MVEC, indicating that activity is present, but that this activity is not extremely high and might be improved.

- 40 [0054] Uninfected MVEC formed capillary-like structures in the fibrin matrices only after stimulation with the TNF-α in combination with bFGF or VEGF. Co-culturing with 10% Ad.IG.CMV.eNOS infected MVEC resulted in an enhanced tube formation, already visible after 5 days. Using cultures existing for 100% of infected cells resulted in less tube formation, probably due to effects of adenoviral infection on the invasive behaviour of these cells, as we have observed previously with other viruses.

- 45 After 7 days, the experiment was stopped, tube formation was analysed visually and quantified by image analysis (see figure 4).

- Tube formation was clearly enhanced in the presence of 10% Ad.IG.CMV.eNOS infected MVEC, even in cultures stimulated only with TNF-α. The strongest induction, 2.1 fold, can be seen in the VEGF+TNF-α stimulated cultures. In the bFGF+TNF-α stimulated cultures a 1.65 fold induction by eNOS overexpression was observed. In the cultures existing
- 50 for 100% of infected cells the tube formation, although present, is less pronounced than the 10% cultures when analysed by image analysis for total tube length. However, the number of starting sprouts is clearly increased in the 100% cultures. In the bFGF+TNF-α stimulated cultures it can be seen that addition of L-NAME (100 μM), an inhibitor of NOS activity, resulted in a small reduction of tube formation, not only in the presence of NOS infected cells but also under normal conditions. This might suggest that endogenous NOS activity is already involved in the process leading to tube
- 55 formation. It can be concluded that infection with Ad.IG.CMV.eNOS has an enhancing effect on *in vitro* angiogenesis c.q. capillary-like tube information in fibrin matrices.

Especially the enhancing effect on tube formation of eNOS overexpression in the VEGF stimulated cultures is very interesting, since the dose of VEGF used, 25 ng/ml, is known to give maximal induction of tube formation in the test

system (figure 5).

Example 8

- 5 [0055] Improved angiogenesis in mice following administration of Ad.IG.CMV.eNOS.
 [0056] A murine model of operatively induced hindlimb ischemia was used to investigate the impact of gene therapy to promote angiogenesis. Hindlimb ischemia was induced in 20 mice according to Murohara T et al (Murohara T., et. al., 1998, J. Clin. Invest. 101, pp 2567-2578). Sixteen mice were divided into 4 groups of 4 mice which were injected with 10^6 , 10^7 , 10^8 , 10^9 pfu Ad.IG.CMV.eNOS, respectively. Four mice received an injection with PBS and served as
 10 negative controls. Upon evaluation of the mice by laser Doppler flow analysis and capillary density measurement (Murohara T., et. al., 1998, J. Clin. Invest. 101, pp 2567-2578) we observed a dose dependent increase in angiogenesis compared to PBS injected control mice.

CITED LITERATURE

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Table 1

Number of colonies after transfection of PER.C6 with E2A expression vectors:		
plasmid	number of colonies	cell lines established
pcDNA3	~200	4/4
PcDNA3wtE2A	4	1/4
PcDNA3tsE2A	~100	37/45

Table 2

PER.C6tsE2A C3-9 and parental PER.C6 infection with dl802 (Ad2 deleted in E2A gene) or IG.Ad.CMV.LacZ at 32°C.		
cell line infected	CPE with IG.Ad.CMV.LacZ	CPE with dl802
PER.C6	+	-
PER.C6.ts125E2A	+	+

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Introgene B.V.
- (B) STREET: Wassenaarseweg 72
- (C) CITY: Leiden
- (D) STATE: Zuid-Holland
- (E) COUNTRY: the Netherlands
- (F) POSTAL CODE (ZIP): 2333 AL

(ii) TITLE OF INVENTION: Gene therapy to promote angiogenesis.

(iii) NUMBER OF SEQUENCES: 24

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 98204482.8

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCCTCATGAA CTTTCTGCTG T
21

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AAAGTCGACT CTAGATCAGC TCATCTCTCC TATCTGC
37

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CGGGATCCGC CACCATGGCC AGTCGGGAAG AGGAG
35

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGGAATTCTT AAAAATCAAA GGGGTTCTGC CGC
33

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTGTCTTA ATTAACCGCT TAA
23

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AATTGTCTTA ATTAACCGC
19

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AATTGCGGTT AATTAAGAC
19

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGCGTACGTA GCCCTGTCGA AAG
23

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCAATGCATT CGAAGTACTT CCTTCTC
27

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCAATGCATA CGGCGCAGAC GG
22

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGGTGGATC CCATGGACGA G
21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGGGGATCCG AACTTGTTTA TTGCAGC

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGGAGATCTA GACATGATAA GATAC
25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGGAGATCTG TACTGAAATG TGTGGGC
27

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGAGGCTGCA GTCTCCAACG GCGT
24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
CTGTACGTAC CAGTGCACTG GCCTAGGCAT GGAAAAATAC ATAAC TG
47

15 (2) INFORMATION FOR SEQ ID NO: 17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
GCGGATCCTT CGAACCATGG TAAGCTTG GT ACCGCTAGCG TTAACCGGGC GACTCAGTCA
60
30 ATCG
64

(2) INFORMATION FOR SEQ ID NO: 18:
(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
40 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
45 GCGCCACCAT GGGCAGAGCG ATGGTGGC
28

(2) INFORMATION FOR SEQ ID NO: 19:
(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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GTTAGATCTA AGCTTGTCGA CATCGATCTA CTAACAGTAG AGATGTAGAA
50

(2) INFORMATION FOR SEQ ID NO: 20:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

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TTAAGTCGAC
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(2) INFORMATION FOR SEQ ID NO: 21:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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GCGTATTAGG CCAAAGGCGC
20

(2) INFORMATION FOR SEQ ID NO: 22:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GATCCCATGG AAGCTTGGGT GGCGACCCCA GCG
33

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GATCCCATGG GGATCCTTTA CTAAGTTACA AAGCTA
36

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTCGCTGTAG TTGGACTGG
19

Claims

1. A nucleic acid delivery vehicle for enhancing and/or inducing angiogenesis, comprising a nucleic acid comprising at least one sequence coding for a protein capable of increasing nitric oxide production, and further comprising a nucleic acid delivery carrier.
2. A nucleic acid delivery vehicle according to claim 1, wherein said sequence codes for a nitric oxide synthetase or a functional analogue or a derivative thereof.
3. A nucleic acid delivery vehicle according to claim 1 or claim 2, further comprising at least one sequence encoding an additional angiogenesis promoting factor.
4. A nucleic acid delivery vehicle according to claim 3, wherein said additional angiogenesis promoting factor is VGEF,

bFGF, angiopoietin-1, or functional analogues or derivatives thereof.

5. A nucleic acid delivery vehicle according to anyone of claims 1-4, wherein the expression of at least one sequence is regulated by a signal.
6. A nucleic acid delivery vehicle according to claim 5, wherein said signal is provided by the oxygen tension in a cell.
7. A nucleic acid delivery vehicle according to claim 5 or claim 6, wherein at least one sequence is expressed from a hypoxia inducible factor 1 α promoter.
8. A nucleic acid delivery vehicle according to anyone of claims 1-7, further comprising a sequence encoding a herpes simplex virus thymidine kinase or a functional analogue or a derivative thereof.
9. A nucleic acid delivery vehicle according to anyone of claims 1-8, wherein said nucleic acid delivery carrier comprises an adenovirus vector or an adeno-associated virus vector.
10. A nucleic acid delivery vehicle according to anyone of claims 1-9, wherein said nucleic acid delivery vehicle has been provided with a least a partial tissue tropism for muscle cells.
11. A nucleic acid delivery vehicle according to anyone of claims 1-10, wherein said nucleic acid delivery vehicle has been at least in part deprived of a tissue tropism for liver cells.
12. A nucleic acid delivery vehicle according to claim 10 or claim 11, wherein said tissue tropism is provided at least in part through a tissue tropism determining part of fiber protein of a subgroup B adenovirus.
13. A nucleic acid delivery vehicle according to claim 12, wherein said subgroup B adenovirus is adenovirus 16.
14. A method for enhancing and/or inducing angiogenesis comprising providing cells of an individual with a nucleic acid delivery vehicle according to anyone of claims 1-13.
15. A method according to claim 14 for enhancing and/or inducing angiogenesis in a synergistic fashion with at least one additional angiogenesis promoting factor or parts or derivatives or functional analogues thereof.
16. A method according to claim 14 or claim 15, wherein the said enhancing and/or inducing angiogenesis effect is at least in part reversible.
17. A method according to claim 16, wherein said effect is at least in part reversed though an increase in the oxygen tension or through providing said cells with gancyclovir or functional analogue thereof, or both.
18. A method according to anyone of claims 14-17, wherein said cells comprise at least cells that under normal circumstances are not in direct contact with blood.
19. A method according to claim 18, wherein said cells are muscle cells.
20. A method according to claim 18 or claim 19 wherein said cells are smooth muscle cells.
21. The use of a nucleic acid delivery vehicle according to anyone of claims 1-13 or a method according to anyone of claims 14-20 for the treatment of endothelial dysfunction.
22. A cell for the production of a nucleic acid delivery vehicle according to anyone of claims 9-13 comprising means for the production of said virus vector in the absence of replication competent adenovirus and adeno-associated virus.
23. A cell according to claim 22, wherein said cell expresses at least one means for the production of said virus vector from a nucleic acid integrated in the chromosomal DNA of said cell and expresses other means for the production of said virus vector from nucleic acid not integrated in the chromosomal DNA of said cell and wherein said integrated nucleic acid and said non-integrated nucleic acid do not comprise sequence overlap leading to the formation of replication competent adenovirus.

24. A cell according to claim 23, wherein said integrated nucleic acid comprises at least an adenovirus E1-region or a functional analogue or a derivative thereof.

5 25. A cell according to claim 23 or claim 24, wherein said integrated nucleic acid comprises at least a sequence encoding an adenovirus E2A protein, preferably an E2A-protein derived from adenovirus ts125 or functional analogues or derivatives thereof.

10 26. A cell according to anyone of claims 22-25, wherein said integrated nucleic acid comprises at least an adenovirus E4-region, preferably E4-orf6, or a functional analogue or a derivative thereof.

27. A cell according to anyone of claims 22-26, wherein said cell is derived from a PER.C6 cell (ECACC deposit number 96022940).

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PER.C6 growth curve

Figure 1

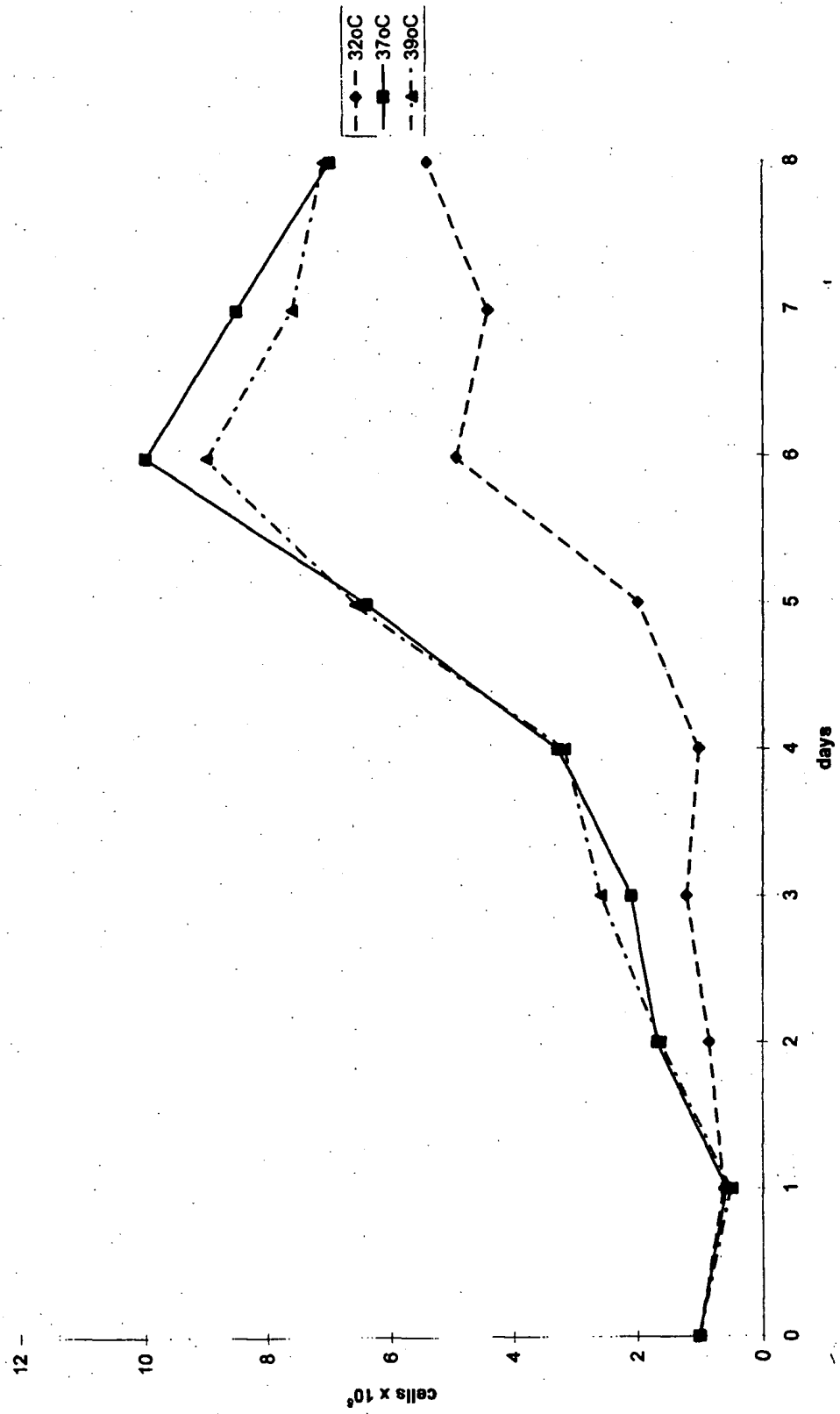


Figure 2

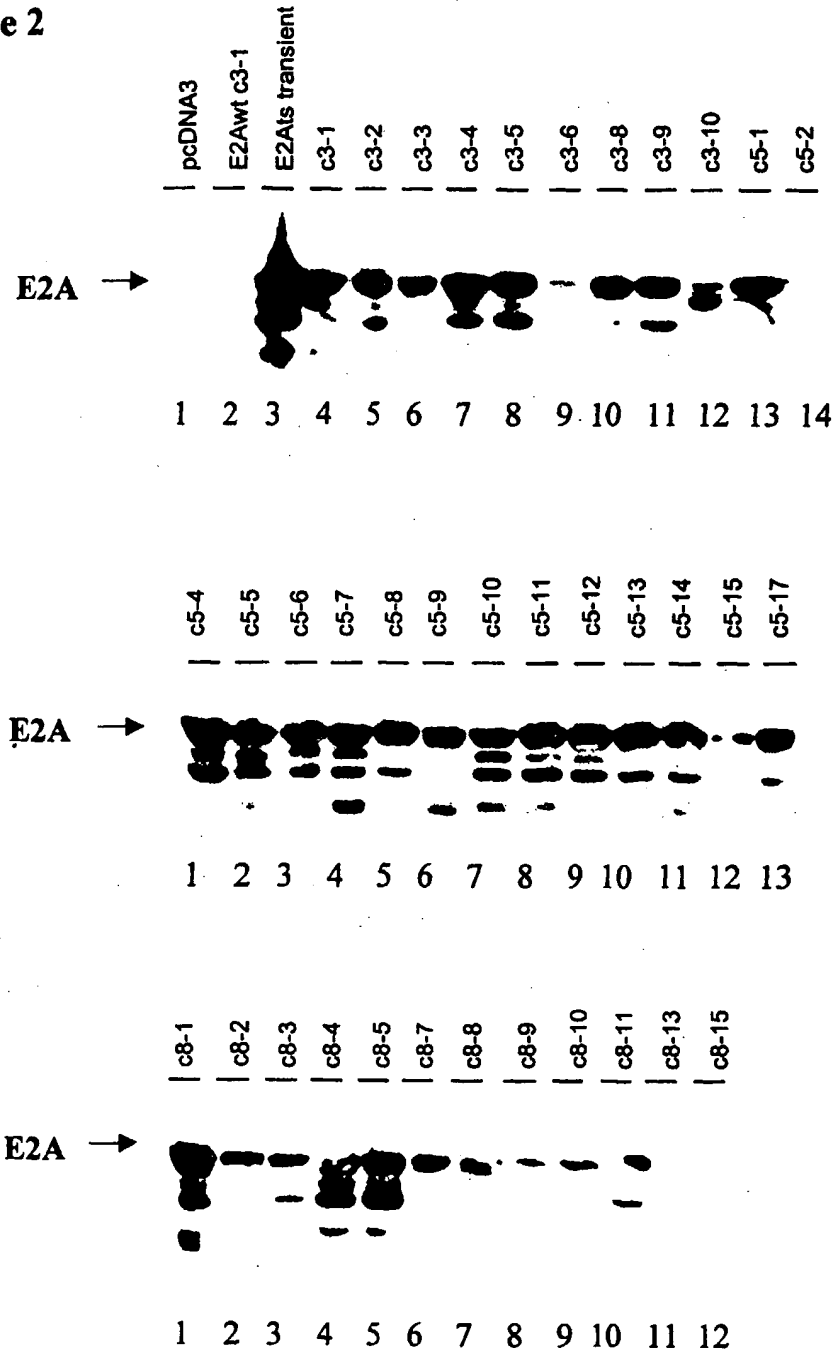
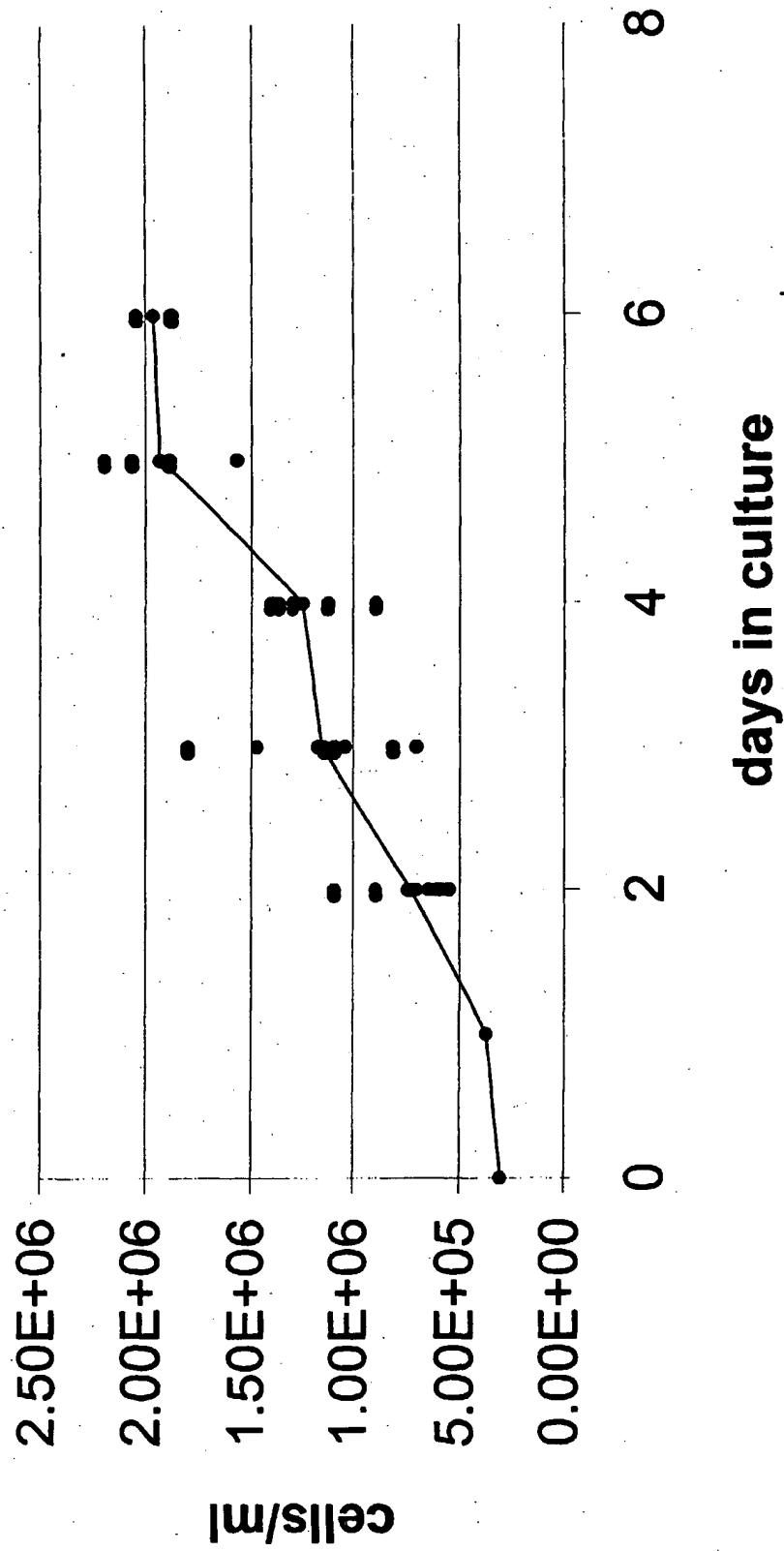


Figure 3: Suspension growth of PER.C6ts125E2A C5-9



Infection of MVEC with Ad.IG.CMV.eNOS

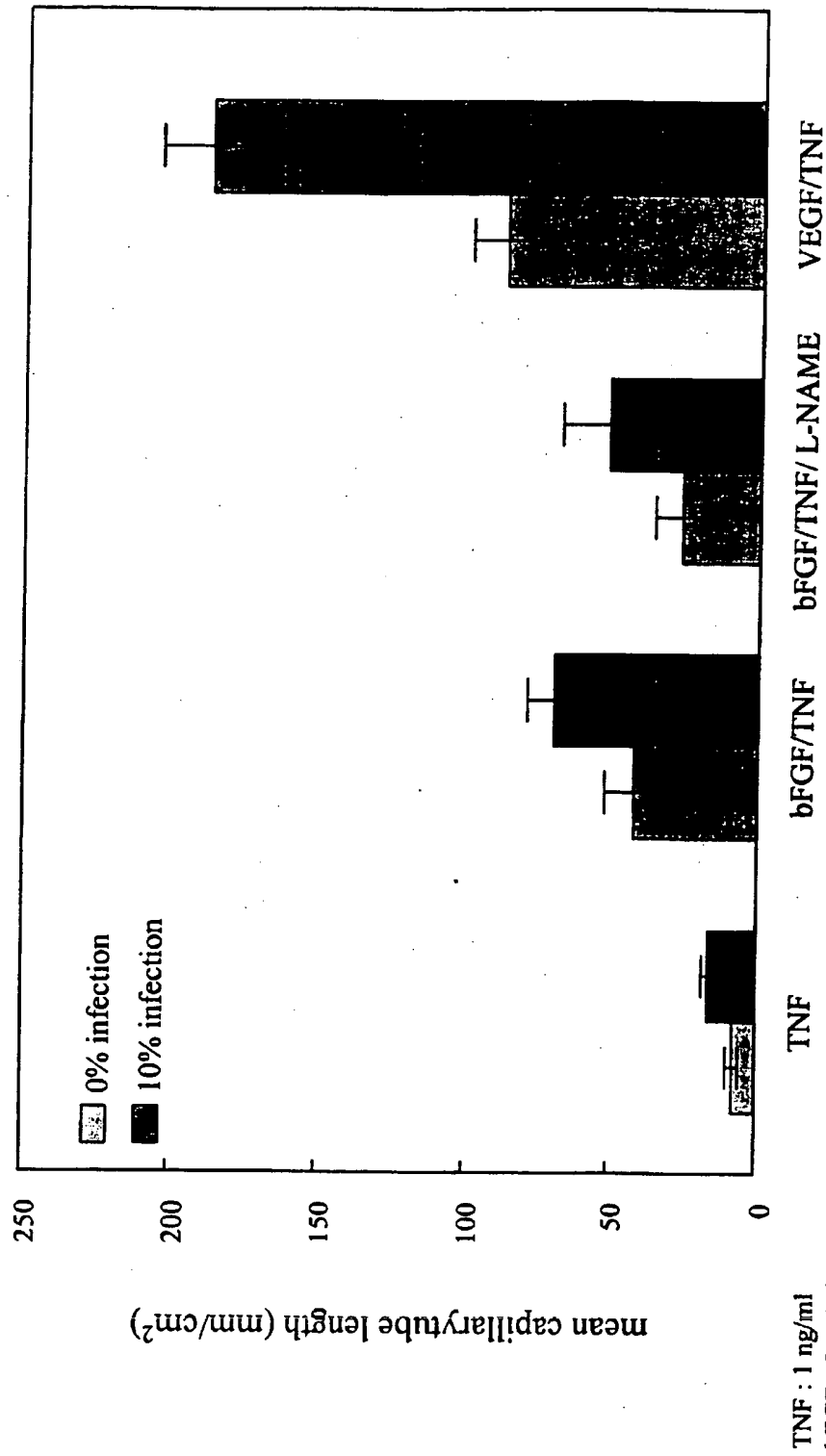
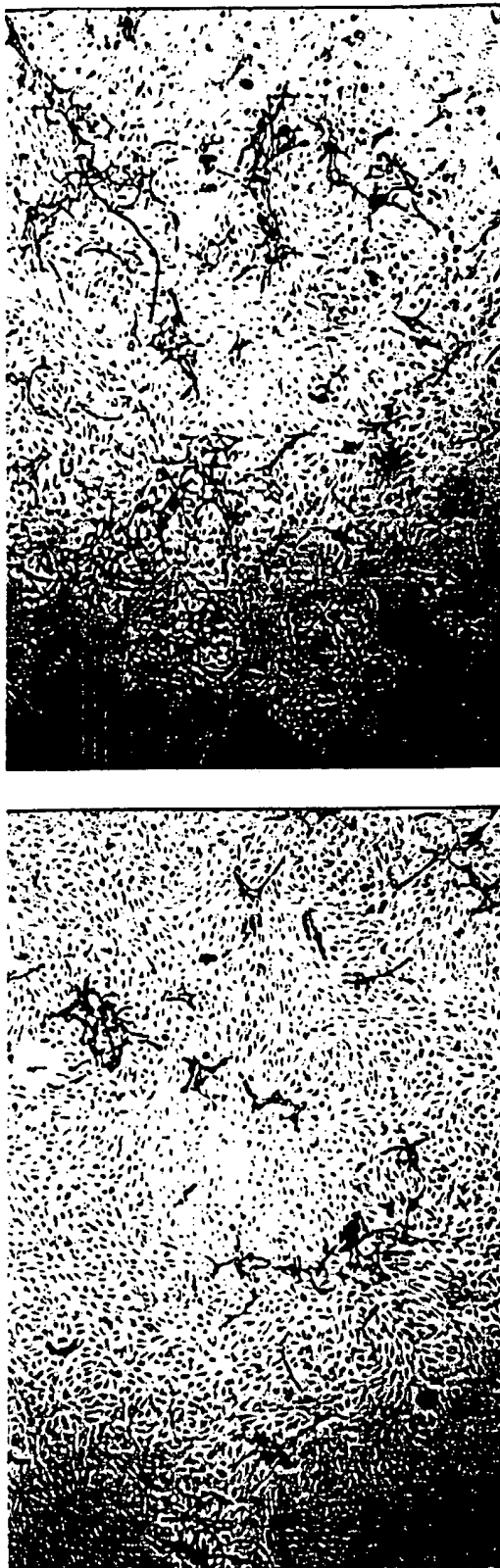


Figure 4

Effect of 10% Ad.IG.CMV.NOS infected
MVEC on angiogenesis



VEGF

VEGF+eNOS

Figure 5



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention EP 98 20 4482 shall be considered, for the purposes of subsequent proceedings, as the European search report

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
X	SHEARS L L 2ND ET AL: "Efficient inhibition of intimal hyperplasia by adenovirus -mediated inducible nitric oxide synthase gene transfer to rats and pigs in vivo." JOURNAL OF THE AMERICAN COLLEGE OF SURGEONS, (1998 SEP) 187 (3) 295-306. , XP002111674	1,2,5,9, 14,16, 18-21	C12N15/86 C12N15/53 C12N9/02 C12N5/10 A61K48/00
Y	* abstract; figures 2-4; table 1 * ---	3,4,8	
X	JANSSENS S ET AL: "Human endothelial nitric oxide synthase gene transfer inhibits vascular smooth muscle cell proliferation and neointima formation after balloon injury in rats." CIRCULATION, (1998 APR 7) 97 (13) 1274-81. , XP002111675	1,2,14, 18-21	
Y	* abstract; figures 2,4 * ---	3,4,8	
			TECHNICAL FIELDS SEARCHED (Int.Cl.7)
			C12N A61K
INCOMPLETE SEARCH			
<p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely:</p> <p>Claims searched incompletely:</p> <p>Claims not searched:</p> <p>Reason for the limitation of the search:</p> <p>Although claims 14-21 are directed to a method of treatment of the human/animal body (Article 52(4) EPC), the search has been carried out and based on the alleged effects of the compound/composition.</p>			
Place of search		Date of completion of the search	Examiner
THE HAGUE		23 August 1999	Espen, J
CATEGORY OF CITED DOCUMENTS			
<p>X : particularly relevant if taken alone</p> <p>Y : particularly relevant if combined with another document of the same category</p> <p>A : technological background</p> <p>O : non-written disclosure</p> <p>P : intermediate document</p>		<p>T : theory or principle underlying the invention</p> <p>E : earlier patent document, but published on, or after the filing date</p> <p>D : document cited in the application</p> <p>L : document cited for other reasons</p> <p>.....</p> <p>& : member of the same patent family, corresponding document</p>	

EPO FORM 1503 (03.92) (P04007)



European Patent
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PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 98 20 4482

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
Y	LAITINEN M ET AL: "Vascular gene transfer for the treatment of restenosis and atherosclerosis." CURRENT OPINION IN LIPIDOLOGY, (1998 OCT) 9 (5) 465-9. REF: 61, XP002111676 * abstract; table 1 *	3,4,8	
Y	WITZENBICHLER B ET AL: "Vascular endothelial growth factor -C (VEGF -C/ VEGF -2) promotes angiogenesis in the setting of tissue ischemia." AMERICAN JOURNAL OF PATHOLOGY, (1998 AUG) 153 (2) 381-94. , XP002111677 * abstract *	3,4	
X	FALLAUX F J ET AL: "New helper cells and matched early region 1-deleted adenovirus vectors prevent generation of replication-competent adenoviruses." HUMAN GENE THERAPY, (1998 SEP 1) 9 (13) 1909-17. , XP002111678 * abstract; figure 1 *	22-24	TECHNICAL FIELDS SEARCHED (Int.Cl.7)



European Patent
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Application Number

EP 98 20 4482

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

- ☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):
- ☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

- ☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.
- ☒ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.
- ☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:
- ☐ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:



European Patent
Office

**LACK OF UNITY OF INVENTION
SHEET B**

Application Number
EP 98 20 4482

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: 1-20

Enhancing and/or inducing angiogenesis with the aid of nucleic acid delivery vehicle comprising a sequence coding for nitric oxid synthetase

2. Claims: 22-27

Adenovirus helper cell, said cell being derived from a PER.C6 cell

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